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G. Mitchell

SD9

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/455,486

DATE: 02/05/2001
TIME: 13:12:57

Input Set : A:\129.17-US-II SEQLIST - 2000-01-12.TXT
Output Set: N:\CRF3\02052001\1455486.raw

```

4 <110> APPLICANT: Daniel E. Afar
5      Rene S. Hubert
6      Arthur B. Raitano
7      Douglas C. Saffran
8      Stephen C. Mitchell
10 <120> TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
11      EXPRESSED IN HUMAN CANCERS AND USES THEREOF
14 <130> FILE REFERENCE: 129.17-US-II
16 <140> CURRENT APPLICATION NUMBER: 09/455,486
17 <141> CURRENT FILING DATE: 1999-12-06
19 <150> PRIOR APPLICATION NUMBER: 09/323,873
20 <151> PRIOR FILING DATE: 1999-06-01
22 <160> NUMBER OF SEQ ID NOS: 34
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1193
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (64)...(1083)
35 <400> SEQUENCE: 1
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37 tta atg gaa aac aca aac caa gaa ctt tgg aaa 108
38      Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys
39      1           5           10          15
41 atg aag cct agg aca aat tta gaa gac gat tat ttg cat aag gac 156
42 Met Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp
43      20          25          30
45 acg gga gag acc agc atg cta aaa aga cct gtg ctt ttg cat ttg cac 204
46 Thr Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His
47      35          40          45
49 caa aca gcc cat gtc gat gaa ttt gac tgc cct tca gaa ctt cag cac 252
50 Gln Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His
51      50          55          60
53 aca cag gaa ctc ttt cca caq tgg cac ttg cca att aaa ata gct gct 300
54 Thr Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala
55      65          70          75
57 att ata gca tct ctg act ttt ctt tac act ctt ctg agg gaa gta att 348
58 Ile Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile
59      80          85          90          95
61 cac cct tta gca act tcc cat caa caa tat ttt tat aaa att cca atc 396
62 His Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile
63      100         105         110
65 ctg gtc atc aac aaa gtc ttg cca atg gtt tcc atc act ctc ttg gca 444
66 Leu Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala
67      115         120         125

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Input Set : A:\129.17-US-II SEQLIST - 2000-01-12.TXT
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69	ttg	gtt	tac	ctg	cca	ggt	gtg	ata	gca	gca	att	gtc	caa	ctt	cat	aat		492	
70	Leu	Val	Tyr	Leu	Pro	Gly	Val	Ile	Ala	Ala	Ile	Val	Gln	Leu	His	Asn			
71								130			135				140				
73	gga	acc	aag	tat	aag	aag	ttt	cca	cat	tgg	ttg	gat	aag	tgg	atg	tta		540	
74	Cly	Thr	Lys	Tyr	Lys	Lys	Phe	Pro	His	Trp	Leu	Asp	Lys	Trp	Met	Leu			
75								145			150				155				
77	aca	aga	aag	cag	ttt	ggg	ctt	ctc	agt	ttc	ttt	ttt	gtc	gta	ctg	cat		588	
78	Thr	Arg	Lys	Gln	Phe	Gly	Leu	Leu	Ser	Phe	Phe	Phe	Ala	Val	Leu	His			
79	160						165				170					175			
81	gca	att	tat	agt	ctg	tct	tac	cca	atg	agg	cga	tcc	tac	aga	tac	aag		636	
82	Ala	Ile	Tyr	Ser	Leu	Ser	Tyr	Pro	Met	Arg	Arg	Ser	Tyr	Arg	Tyr	Lys			
83							180			185					190				
85	ttg	cta	aac	tgg	gca	tat	caa	cag	gtc	caa	caa	aat	aaa	gaa	gat	gcc		684	
86	Leu	Leu	Asn	Trp	Ala	Tyr	Gln	Gln	Val	Gln	Gln	Asn	Lys	Glu	Asp	Ala			
87						195			200					205					
89	tgg	att	gag	cat	gat	gtt	tgg	aga	atg	gag	att	tat	gtg	tct	ctg	gga		732	
90	Trp	Ile	Glu	His	Asp	Val	Trp	Arg	Met	Glu	Ile	Tyr	Val	Ser	Leu	Gly			
91						210			215				220						
93	att	gtg	gga	ttg	gca	ata	ctg	gct	ctg	ttg	gct	gtg	aca	tct	att	cca		780	
94	Ile	Val	Gly	Leu	Ala	Ile	Leu	Ala	Leu	Leu	Ala	Val	'Thr	Ser	Ile	Pro			
95						225			230				235						
97	tct	gtg	agt	gac	tct	ttg	aca	tgg	aga	gaa	ttt	cac	tat	att	cag	agc		828	
98	Ser	Val	Ser	Asp	Ser	Leu	Thr	Trp	Arg	Glu	Phe	His	Tyr	Ile	Gln	Ser			
99	240					245				250					255				
101	aag	cta	gga	att	gtt	tcc	ctt	cta	ctg	ggc	aca	ata	cac	gca	ttg	att		876	
102	Lys	Leu	Gly	Ile	Val	Ser	Leu	Leu	Leu	Gly	Thr	Ile	His	Ala	Leu	Ile			
103						260			265				270						
105	ttt	gcc	tgg	aat	aag	tgg	ata	gat	ata	aaa	caa	ttt	gta	tgg	tat	aca		924	
106	Phe	Ala	Trp	Asn	Lys	Trp	Ile	Asp	Ile	Lys	Gln	Phe	Val	Trp	Tyr	Thr			
107						275			280				285						
109	cct	cca	act	ttt	atg	ata	gtc	ttt	cca	att	gtt	gtc	ctg	ata				972	
110	Pro	Pro	Thr	Phe	Met	Ile	Ala	Val	Phe	Leu	Pro	Ile	Val	Val	Leu	Ile			
111						290			295				300						
113	ttt	aaa	agc	ata	cta	ttc	ctg	cca	tgc	ttg	agg	aag	aag	ata	ctg	aag		1020	
114	Phe	Lys	Ser	Ile	Leu	Phe	Leu	Pro	Cys	Leu	Arg	Lys	Lys	Ile	Leu	Lys			
115						305			310				315						
117	att	aga	cat	ggt	tgg	gaa	gac	gtc	acc	aaa	att	aac	aaa	act	gag	ata		1068	
118	Ile	Arg	Ile	Gly	Trp	Glu	Asp	Val	Thr	Lys	Ile	Asn	Lys	Thr	Glu	Ile			
119	320					325				330				335					
121	tgt	tcc	cag	ttg	tag	aattactgtt	tacacacat	t	tttgttcaat	attgtatata								1123	
122	Cys	Ser	Gln	Leu	*														
125	tttatcacca	acatttcaag	tttgttatttg	ttaataaaat	gattattcaa	ggaaaaaaaaaa												1183	
126	aaaaaaaaaaaa																	1193	
128	<210>	SEQ ID NO:	2																
129	<211>	LENGTH:	339																
130	<212>	TYPE:	PRT																
131	<213>	ORGANISM:	Homo sapiens																
133	<400>	SEQUENCE:	2																
134	Met	Glu	Ser	Arg	Lys	Asp	Ile	Thr	Asn	Gln	Glu	Leu	Trp	Lys	Met				

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Output Set: N:\CRF3\02052001\I455486.raw

```

135 1      5      10      15
136 Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
137      20      25      30
138 Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
139      35      40      45
140 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
141      50      55      60
142 Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
143 65      70      75      80
144 Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
145      85      90      95
146 Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
147      100     105     110
148 Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
149      115     120     125
150 Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
151      130     135     140
152 Thr Lys Tyr Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
153 145     150     155     160
154 Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Ala Val Leu His Ala
155      165     170     175
156 Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
157      180     185     190
158 Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
159      195     200     205
160 Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
161      210     215     220
162 Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
163 225     230     235     240
164 Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
165      245     250     255
166 Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
167      260     265     270
168 Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
169      275     280     285
170 Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
171      290     295     300
172 Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
173 305     310     315     320
174 Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys
175      325     330     335
176 Ser Gln Leu
179 <210> SEQ ID NO: 3
180 <211> LENGTH: 111
181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 3
185 ggcggaggcg gagggcggagg gcgaggggcg gggagcgccg cctggagcgc ggcaggcat      60
186 attgaacatt ccagataacct atcattactc gatgtgttg ataacagcaa g      111

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RAW SEQUENCE LISTING DATE: 02/05/2001
PATENT APPLICATION: US/09/455,486 TIME: 13:32:57

Input Set : A:\129.17-US-II SEQLIST - 2000-01-12.TXT
Output Set: N:\CRF3\02052001\I455486.raw

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/455,486

DATE: 02/05/2001
TIME: 13:12:57

Input Set : A:\129.17-US-II SEQLIST - 2000-01-12.TXT
Output Set: N:\CRF3\02052001\I455486.raw

238	cataattttt	ccatgttato	agaatatttg	attttttaaa	aacataggcc	aagttcattc	2700
239	acttcattat	tcatttatca	aaatcagagt	gaatcacat	agtgccttc	acaactgata	2760
240	aagatcactg	augcaaaatt	gatttttgt	ataatcttca	atctacctat	atttaaattga	2820
241	gaatctaaaa	tgtacaaatc	attgtgttga	ttctgcagtg	atcctgttat	aatgttttttt	2880
242	cagtccttga	tittaggtat	cctgtaaaaa	gcagaattaa	gacaaataca	caagagacaa	2940
243	agcacaaaaa	ataaaatatca	taagggatg	aacaaaatgg	tggagaaaaga	gttagacaaag	3000
244	tttttgcata	ccttccttca	aagaaaggct	gtgaattttt	ttcactttaga	cagcttggag	3060
245	acaagaattt	accaaaaagt	aagggtgagga	ggtataggcaa	aaagagcaga	aagatgtgaa	3120
246	tggacatgt	tgagauatgt	gatagaaaaa	caatcataga	taaaggattt	ccaagcaaca	3180
247	gagcatatcc	agatgaggta	ggatggata	aacttttatt	gaaccaatct	tcaccaattt	3240
248	tgtttttctt	ttgcagagca	agcttagaat	tgtttccctt	ctactggca	caatacacgc	3300
249	attgattttt	cccttggata	agtggataga	tataaaacaa	tttgtatggt	atacaccc	3360
250	aactttatg	atagctgttt	tccttccat	tgttgtcctg	atatttaaaa	gcataactatt	3420
251	cctgcctatgc	ttgaggaaga	agatactgaa	gattagacat	ggttgggaag	acgtcaccaa	3480
252	aattaacaaa	actgagatat	gttcccagt	gttagaattac	tgtttacaca	cattttgtt	3540
253	caatattgtat	atattttatc	accaacattt	caagtttgc	tttgttaata	aaatgattat	3600
254	tcaaggaaaa	aaaaaaaaa	aaaaaaa	aaaaaaa			3627
256	<210>	SEQ ID NO:	5				
257	<211>	LENGTH:	2453				
258	<212>	TYPE:	DNA				
259	<213>	ORGANISM:	Homo sapiens				
261	<220>	FEATURE:					
262	<221>	NAME/KEY:	CDS				
263	<222>	LOCATION:	(355)...(1719)				
265	<400>	SEQUENCE:	5				
266	ggacgcgtgg	ggggacgcgt	gggttcctcg	ggccctcgyc	gccacaagct	gtccccggcac	60
267	geagecccta	ggggggggc	gttgcacaa	cgccctccgc	ggccctccct	cetttcttct	120
268	ccccctggctq	ttcgcgatcc	agtttggta	ggggggggaaq	cagctggagt	gcgacccgca	180
269	cggcacccac	cctgcacaccq	ccagtcggag	gtgcagtcgg	tagccctgg	ccccgggtg	240
270	ggcccttggg	gatggggggc	cgctcccgag	gagctycaag	gtctggccct	ggccggcggt	300
271	gagggcgcgg	ggggggggg	ggatattttt	ggtgatcttq	gaagtgtccg	tatc atg	357
272					Met		
273					1		
275	gaa tca atc tct atg	atg gga	agc ect	aaq agc ctt	agt gaa	act tgt	405
276	Glu Ser Ile Ser Met	Met Gly Ser Pro Lys	Ser Leu Ser	Glu Thr Cys			
277	5	10	15				
279	tta cct aat ggc	ata aat ggt	atc aaa	gat gca	agg aag	gtc act gta	453
280	Leu Pro Asn Gly	Ile Asn Gly	Ile Lys Asp	Ala Arg Lys	Val Thr Val		
281	20	25	30				
283	ggt gtg att gga	agt gga	gat ttt	gcc aaa	tcc ttg	acc att cga	501
284	Gly Val Ile Gly	Ser Gly Asp Phe	Ala Lys Ser	Leu Thr Ile Arg	Leu		
285	35	40	45				
287	att aga tgc ggc	tat cat gtg	gtc ata gga	agt aga	aat cct	aag ttt	549
288	Ile Arg Cys Gly	Tyr His Val Val	Ile Gly Ser	Arg Asn Pro	Lys Phe		
289	50	55	60	65			
291	gct tct gaa ttt	ttt cct cat	gtg gta	gat gtc	act cat	cat gaa	597
292	Ala Ser Glu Phe	Phe Pro His Val Val	Asp Val Thr	His His Glu	Asp		
293	70	75	80				
295	gct ctc aca	aaa aca	aat ata	ata ttt	gtt gct	ata cac aga	645

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/455,486

DATE: 02/05/2001
TIME: 13:12:58

Input Set : A:\129.17-US-II SEQLIST - 2000-01-12.TXT
Output Set: N:\CRF3\02052001\I455486.raw

L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:782 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:782 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:782 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
L:784 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:784 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:790 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:790 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:794 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:794 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:796 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:796 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:798 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:798 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13